SEQUENCE LISTING

<110> Hyseq, Inc.

<120> A NOVEL EGF MOTIF PROTEIN OBTAINED FROM
A cDNA LIBRARY OF FETAL LIVER-SPLEEN

<130> 20411-720

<140> US 08/968,800
<141> 1997-11-22

<160> 20

<170> FastSEQ for Windows Version 3.0

<210> 1
<211> 300
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)...(300)

<221> misc_feature
<222> (1)...(300)
<223> n = A,T,C or G

a'

<400> 1

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ggc tgg aga aga aac agc aag gga gtc tgt gaa gct aca tgc gaa cct       48
Gly Trp Arg Arg Asn Ser Lys Gly Val Cys Glu Ala Thr Cys Glu Pro
 1               5                  10                  15

gga tgt aag ttt ggt gag tgc gtg gga cca aac aaa tgc aga tgc ttt       96
Gly Cys Lys Phe Gly Glu Cys Val Gly Pro Asn Lys Cys Arg Cys Phe
            20                  25                  30

cca gga tac acc ggg aaa acc tgc agt caa gat gtg aat gag tgt gga      144
Pro Gly Tyr Thr Gly Lys Thr Cys Ser Gln Asp Val Asn Glu Cys Gly
        35                  40                  45

atg aaa ccc cgg cca tgc caa cac aga tgt gtg aat aca cac gga agc      192
Met Lys Pro Arg Pro Cys Gln His Arg Cys Val Asn Thr His Gly Ser
    50                  55                  60
```

```
tac aag tgc ttt tgc ctc agt ggc cac atg ctc atg cca gat gct acg      240
Tyr Lys Cys Phe Cys Leu Ser Gly His Met Leu Met Pro Asp Ala Thr
 65                  70                  75                  80

tgt gtg aac tcn agg aca tgt gcc atg ata aac tgt cag tat agc tgt      288
Cys Val Asn Xaa Arg Thr Cys Ala Met Ile Asn Cys Gln Tyr Ser Cys
                 85                  90                  95

gaa gac aca gaa                                                     300
Glu Asp Thr Glu
            100
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<210> 2
<211> 1611
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)...(1506)

<221> misc_feature
<222> (1)...(1611)
<223> n = A,T,C or G

<400> 2

a1 cont.

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ggc tgg aga aga aac agc aag gga gtc tgt gaa gct aca tgc gaa cct       48
Gly Trp Arg Arg Asn Ser Lys Gly Val Cys Glu Ala Thr Cys Glu Pro
 1               5                  10                  15

gga tgt aag ttt ggt gag tgc gtg gga cca aac aaa tgc aga tgc ttt       96
Gly Cys Lys Phe Gly Glu Cys Val Gly Pro Asn Lys Cys Arg Cys Phe
            20                  25                  30

cca gga tac acc ggg aaa acc tgc agt caa gat gtg aat gag tgt gga      144
Pro Gly Tyr Thr Gly Lys Thr Cys Ser Gln Asp Val Asn Glu Cys Gly
        35                  40                  45

atg aaa ccc cgg cca tgc caa cac aga tgt gtg aat aca cac gga agc      192
Met Lys Pro Arg Pro Cys Gln His Arg Cys Val Asn Thr His Gly Ser
    50                  55                  60

tac aag tgc ttt tgc ctc agt ggc cac atg ctc atg cca gat gct acg      240
Tyr Lys Cys Phe Cys Leu Ser Gly His Met Leu Met Pro Asp Ala Thr
 65                  70                  75                  80
```

```
tgt gtg aac tcn agg aca tgt gcc atg ata aac tgt cag tat agc tgt      288
Cys Val Asn Xaa Arg Thr Cys Ala Met Ile Asn Cys Gln Tyr Ser Cys
                 85                  90                  95

gaa gac aca gaa gaa ggg cca cag tgc ctg tgt cca tcc tca gga ctc      336
Glu Asp Thr Glu Glu Gly Pro Gln Cys Leu Cys Pro Ser Ser Gly Leu
            100                 105                 110

cgc ctg gcc cca aat gga aga gac tgt cta gat att gat gaa tgt gcc      384
Arg Leu Ala Pro Asn Gly Arg Asp Cys Leu Asp Ile Asp Glu Cys Ala
        115                 120                 125

tct ggt aaa gtc atc tgt ccc tac aat cga aga tgt gtg aac aca ttt      432
Ser Gly Lys Val Ile Cys Pro Tyr Asn Arg Arg Cys Val Asn Thr Phe
    130                 135                 140

gga agc tac tac tgc aaa tgt cac att ggt ttc gaa ctg caa tat atc      480
Gly Ser Tyr Tyr Cys Lys Cys His Ile Gly Phe Glu Leu Gln Tyr Ile
145                 150                 155                 160

agt gga cga tat gac tgt ata gat ata aat gaa tgt act atg gat agc      528
Ser Gly Arg Tyr Asp Cys Ile Asp Ile Asn Glu Cys Thr Met Asp Ser
                165                 170                 175

cat acg tgc agc cac cat gcc aat tgc ttc aat acc caa ggg tcc ttc      576
His Thr Cys Ser His His Ala Asn Cys Phe Asn Thr Gln Gly Ser Phe
            180                 185                 190

aag tgt aaa tgc aag cag gga tat aaa ggc aat gga ctt cgg tgt tct      624
Lys Cys Lys Cys Lys Gln Gly Tyr Lys Gly Asn Gly Leu Arg Cys Ser
        195                 200                 205

gct atc cct gaa aat tct gtg aag gaa gtc ctc aga gca cct ggt acc      672
Ala Ile Pro Glu Asn Ser Val Lys Glu Val Leu Arg Ala Pro Gly Thr
    210                 215                 220

atc aaa gac aga atc aag aag ttg ctt gct cac aaa aac agc atg aaa      720
Ile Lys Asp Arg Ile Lys Lys Leu Leu Ala His Lys Asn Ser Met Lys
225                 230                 235                 240

aag aag gca aaa att aaa aat gtt acc cca gaa ccc acc agg act cct      768
Lys Lys Ala Lys Ile Lys Asn Val Thr Pro Glu Pro Thr Arg Thr Pro
                245                 250                 255

acc cct aag gtg aac ttg cag ccc ttc aac tat gaa gag ata gtt tcc      816
Thr Pro Lys Val Asn Leu Gln Pro Phe Asn Tyr Glu Glu Ile Val Ser
            260                 265                 270
```

a' cont

```
aga ggc ggg aac tct cat gga ggt aaa aaa ggg aat gaa gag aaa atg      864
Arg Gly Gly Asn Ser His Gly Gly Lys Lys Gly Asn Glu Glu Lys Met
        275                 280                 285

aaa gag ggg ctt gag gat gag aaa aga gaa gag aaa gcc ctg aag aat      912
Lys Glu Gly Leu Glu Asp Glu Lys Arg Glu Glu Lys Ala Leu Lys Asn
    290                 295                 300

gac ata gag gag cga agc ctg cga gga gat gtg ttt ttc cct aag gtg      960
Asp Ile Glu Glu Arg Ser Leu Arg Gly Asp Val Phe Phe Pro Lys Val
305                 310                 315                 320

aat gaa gca ggt gaa ttc ggc ctg att ctg gtc caa agg aaa gcg cta     1008
Asn Glu Ala Gly Glu Phe Gly Leu Ile Leu Val Gln Arg Lys Ala Leu
                325                 330                 335

act tcc aaa ctg gaa cat aaa gat tta aat atc tcg gtt gac tgc agc     1056
Thr Ser Lys Leu Glu His Lys Asp Leu Asn Ile Ser Val Asp Cys Ser
            340                 345                 350

ttc aat cat ggg atc tgt gac tgg aaa cag gat aga gaa gat gat ttt     1104
Phe Asn His Gly Ile Cys Asp Trp Lys Gln Asp Arg Glu Asp Asp Phe
        355                 360                 365

gac tgg aat cct gct gat cga gat aat gct att ggc ttc tat atg gca     1152
Asp Trp Asn Pro Ala Asp Arg Asp Asn Ala Ile Gly Phe Tyr Met Ala
    370                 375                 380

gtt ccg gcc ttg gca ggt cac atg aaa gac att ggc cga ttg aaa ctt     1200
Val Pro Ala Leu Ala Gly His Met Lys Asp Ile Gly Arg Leu Lys Leu
385                 390                 395                 400

ctc cta cct gac ctg caa ccc caa agc aac ttc tgt ttg ctc ttt gat     1248
Leu Leu Pro Asp Leu Gln Pro Gln Ser Asn Phe Cys Leu Leu Phe Asp
                405                 410                 415

tac cgg ctg gcc gga gac aaa gtc ggg aaa ctt cga gtg ttt gtg aaa     1296
Tyr Arg Leu Ala Gly Asp Lys Val Gly Lys Leu Arg Val Phe Val Lys
            420                 425                 430

aac agt aac aat gcc ctg gca tgg gag aag acc acg agt gag gat gaa     1344
Asn Ser Asn Asn Ala Leu Ala Trp Glu Lys Thr Thr Ser Glu Asp Glu
        435                 440                 445

aag tgg aag aca ggg aaa att cag ttg tat caa gga act gat gct acc     1392
Lys Trp Lys Thr Gly Lys Ile Gln Leu Tyr Gln Gly Thr Asp Ala Thr
    450                 455                 460
```

a1 cont'

```
aaa agc atc att ttt gaa gca gaa cgt ggc aag ggc aaa acc ggc gaa     1440
Lys Ser Ile Ile Phe Glu Ala Glu Arg Gly Lys Gly Lys Thr Gly Glu
465                 470                 475                 480

atc gca gtg gat ggc gtc ttg ctt gtt tca ggc tta tgt cca gat agc     1488
Ile Ala Val Asp Gly Val Leu Leu Val Ser Gly Leu Cys Pro Asp Ser
                485                 490                 495

ctt tta tct gtg gan nnc tgaatggtac tatctttata tttgactttg           1536
Leu Leu Ser Val Xaa Xaa
            500

tatgtcagtt ccctggtttt tttgatattg catcatagga cctctggcat tttaaaatta   1596
ctagctgaaa aattg                                                   1611
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<210> 3
<211> 100
<212> PRT
<213> Homo sapiens

<400> 3

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Gly Trp Arg Arg Asn Ser Lys Gly Val Cys Glu Ala Thr Cys Glu Pro
 1               5                  10                  15
Gly Cys Lys Phe Gly Glu Cys Val Gly Pro Asn Lys Cys Arg Cys Phe
            20                  25                  30
Pro Gly Tyr Thr Gly Lys Thr Cys Ser Gln Asp Val Asn Glu Cys Gly
        35                  40                  45
Met Lys Pro Arg Pro Cys Gln His Arg Cys Val Asn Thr His Gly Ser
    50                  55                  60
Tyr Lys Cys Phe Cys Leu Ser Gly His Met Leu Met Pro Asp Ala Thr
65                  70                  75                  80
Cys Val Asn Ser Arg Thr Cys Ala Met Ile Asn Cys Gln Tyr Ser Cys
                85                  90                  95
Glu Asp Thr Glu
            100
```

a' cont

<210> 4
<211> 537
<212> PRT
<213> Homo sapiens

<220>
<221> VARIANT
<222> (1)...(537)
<223> Xaa = Any Amino Acid

<400> 4

```
Gly Trp Arg Arg Asn Ser Lys Gly Val Cys Glu Ala Thr Cys Glu Pro
 1               5                  10                  15
```

Gly Cys Lys Phe Gly Glu Cys Val Gly Pro Asn Lys Cys Arg Cys Phe
20 25 30
Pro Gly Tyr Thr Gly Lys Thr Cys Ser Gln Asp Val Asn Glu Cys Gly
35 40 45
Met Lys Pro Arg Pro Cys Gln His Arg Cys Val Asn Thr His Gly Ser
50 55 60
Tyr Lys Cys Phe Cys Leu Ser Gly His Met Leu Met Pro Asp Ala Thr
65 70 75 80
Cys Val Asn Ser Arg Thr Cys Ala Met Ile Asn Cys Gln Tyr Ser Cys
85 90 95
Glu Asp Thr Glu Glu Gly Pro Gln Cys Leu Cys Pro Ser Ser Gly Leu
100 105 110
Arg Leu Ala Pro Asn Gly Arg Asp Cys Leu Asp Ile Asp Glu Cys Ala
115 120 125
Ser Gly Lys Val Ile Cys Pro Tyr Asn Arg Arg Cys Val Asn Thr Phe
130 135 140
Gly Ser Tyr Tyr Cys Lys Cys His Ile Gly Phe Glu Leu Gln Tyr Ile
145 150 155 160
Ser Gly Arg Tyr Asp Cys Ile Asp Ile Asn Glu Cys Thr Met Asp Ser
165 170 175
His Thr Cys Ser His His Ala Asn Cys Phe Asn Thr Gln Gly Ser Phe
180 185 190
Lys Cys Lys Cys Lys Gln Gly Tyr Lys Gly Asn Gly Leu Arg Cys Ser
195 200 205
Ala Ile Pro Glu Asn Ser Val Lys Glu Val Leu Arg Ala Pro Gly Thr
210 215 220
Ile Lys Asp Arg Ile Lys Lys Leu Leu Ala His Lys Asn Ser Met Lys
225 230 235 240
Lys Lys Ala Lys Ile Lys Asn Val Thr Pro Glu Pro Thr Arg Thr Pro
245 250 255
Thr Pro Lys Val Asn Leu Gln Pro Phe Asn Tyr Glu Glu Ile Val Ser
260 265 270
Arg Gly Gly Asn Ser His Gly Gly Lys Lys Gly Asn Glu Glu Lys Met
275 280 285
Lys Glu Gly Leu Glu Asp Glu Lys Arg Glu Glu Lys Ala Leu Lys Asn
290 295 300
Asp Ile Glu Glu Arg Ser Leu Arg Gly Asp Val Phe Phe Pro Lys Val
305 310 315 320
Asn Glu Ala Gly Glu Phe Gly Leu Ile Leu Val Gln Arg Lys Ala Leu
325 330 335
Thr Ser Lys Leu Glu His Lys Asp Leu Asn Ile Ser Val Asp Cys Ser
340 345 350
Phe Asn His Gly Ile Cys Asp Trp Lys Gln Asp Arg Glu Asp Asp Phe
355 360 365
Asp Trp Asn Pro Ala Asp Arg Asp Asn Ala Ile Gly Phe Tyr Met Ala
370 375 380
Val Pro Ala Leu Ala Gly His Met Lys Asp Ile Gly Arg Leu Lys Leu
385 390 395 400
Leu Leu Pro Asp Leu Gln Pro Gln Ser Asn Phe Cys Leu Leu Phe Asp
405 410 415

a' cont.

```
Tyr Arg Leu Ala Gly Asp Lys Val Gly Lys Leu Arg Val Phe Val Lys
            420                 425                 430
Asn Ser Asn Asn Ala Leu Ala Trp Glu Lys Thr Thr Ser Glu Asp Glu
        435                 440                 445
Lys Trp Lys Thr Gly Lys Ile Gln Leu Tyr Gln Gly Thr Asp Ala Thr
    450                 455                 460
Lys Ser Ile Ile Phe Glu Ala Glu Arg Gly Lys Gly Lys Thr Gly Glu
465                 470                 475                 480
Ile Ala Val Asp Gly Val Leu Leu Val Ser Gly Leu Cys Pro Asp Ser
                485                 490                 495
Leu Leu Ser Val Asp Asp Xaa Met Val Leu Ser Leu Tyr Leu Thr Leu
            500                 505                 510
Tyr Val Ser Ser Leu Val Phe Leu Ile Leu His His Arg Thr Ser Gly
        515                 520                 525
Ile Leu Lys Leu Leu Ala Glu Lys Leu
    530                 535
```

<210> 5
<211> 42
<212> PRT
<213> Drosophila Melanogaster

<220>
<221> VARIANT
<222> (1)...(42)
<223> Xaa = Any Amino Acid

<400> 5

```
Ile Asp Glu Cys Xaa Ser Asn Pro Cys Gln Asn Gly Gly Thr Cys Xaa
 1               5                  10                  15
Xaa Xaa Asp Xaa Val Gly Ser Tyr Xaa Cys Xaa Cys Pro Pro Gly Phe
            20                  25                  30
Thr Gly Lys Xaa Xaa Xaa Cys Glu Xaa Asn
        35                  40
```

a' cont

<210> 6
<211> 39
<212> PRT
<213> Homo sapiens

<220>
<221> VARIANT
<222> (1)...(39)
<223> Xaa = Any Amino Acid

<400> 6

```
Xaa Asn Glu Cys Thr Met Xaa Xaa Xaa Cys Gln His Xaa Xaa Xaa Cys
 1               5                  10                  15
Val Asn Thr Xaa Gly Ser Tyr Xaa Cys Lys Cys Xaa Ser Gly Xaa Xaa
            20                  25                  30
```

Gly Xaa Xaa Leu Xaa Cys Asp
35

<210> 7
<211> 164
<212> PRT
<213> Homo sapiens

<400> 7

Cys	Arg	Cys	Phe	Pro	Gly	Tyr	Thr	Gly	Lys	Thr	Cys	Ser	Gln	Val	Asn
1				5				10						15	
Glu	Cys	Gly	Met	Lys	Pro	Arg	Pro	Cys	Gln	His	Arg	Cys	Val	Asn	Thr
			20					25					30		
His	Gly	Ser	Tyr	Lys	Cys	Phe	Cys	Leu	Ser	Gly	His	Met	Leu	Met	Pro
		35					40					45			
Asp	Val	Asn	Ser	Arg	Thr	Cys	Ala	Met	Ile	Asn	Cys	Gln	Tyr	Ser	Cys
	50					55					60				
Glu	Asp	Thr	Glu	Glu	Gly	Pro	Gln	Cys	Leu	Cys	Pro	Ser	Ser	Gly	Leu
65					70					75					80
Arg	Leu	Ala	Pro	Asn	Ile	Asp	Glu	Cys	Ala	Ser	Gly	Lys	Val	Ile	Cys
				85					90					95	
Pro	Tyr	Asn	Arg	Arg	Cys	Val	Asn	Thr	Phe	Gly	Ser	Tyr	Tyr	Cys	Lys
			100					105					110		
Cys	His	Ile	Gly	Phe	Glu	Leu	Gln	Tyr	Ile	Ser	Gly	Arg	Ile	Asn	Glu
		115					120					125			
Cys	Thr	Met	Asp	Ser	His	Thr	Cys	Ser	His	His	Ala	Asn	Cys	Phe	Asn
	130					135					140				
Thr	Gln	Gly	Ser	Phe	Cys	Lys	Cys	Lys	Gln	Gly	Tyr	Lys	Gly	Asn	Gly
145					150					155					160
Leu	Arg	Cys	Ser												

<210> 8
<211> 45
<212> PRT
<213> Homo sapiens

a' cont

<220>
<221> VARIANT
<222> (1)...(45)
<223> Xaa = Any Amino Acid

<400> 8

Val	Xaa	Glu	Cys	Xaa	Ser	Gly	Xaa	Gln	Xaa	Xaa	Cys	Xaa	Ser	Ser	Xaa
1				5				10						15	
Xaa	Cys	Xaa	Asn	Thr	Val	Gly	Ser	Tyr	Xaa	Cys	Arg	Cys	Arg	Pro	Gly
			20					25					30		
Trp	Xaa	Pro	Xaa	Pro	Gly	Xaa	Pro	Asn	Xaa	Xaa	Xaa	Asp			
		35					40					45			

<210> 9
<211> 58
<212> PRT
<213> Mammalian

<220>
<221> VARIANT
<222> (1)...(58)
<223> Xaa = Any Amino Acid

<400> 9

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Asn Ser Asp Ser Glu Cys Pro Leu Ser His Asp Gly Tyr Cys Leu His
 1               5                  10                  15
Asp Gly Val Cys Met Tyr Ile Glu Ala Leu Asp Lys Tyr Ala Cys Asn
            20                  25                  30
Cys Val Val Gly Tyr Ile Xaa Xaa Xaa Gly Glu Arg Xaa Xaa Cys Gln
        35                  40                  45
Tyr Arg Asp Leu Lys Trp Trp Glu Leu Arg
    50                  55
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<210> 10
<211> 15
<212> DNA
<213> Artificial Sequence

<220>
<223> Exemplary oligonucleotide primer used in sequence assembly process

<221> misc_feature
<222> (8)...(8)
<223> n = A, T, C, G, or 1-(2-deoxy-D-ribfuranosyl)-3-nitropyrrole

<400> 10
ccttttttntt tttgg 15

a' cont.

<210> 11
<211> 15
<212> DNA
<213> Artificial Sequence

<220>
<223> Exemplary oligonucleotide primer used in sequence assembly process

<221> misc_feature
<222> (8)...(8)
<223> n = A, T, C, G, or 1-(2-deoxy-D-ribfuranosyl)-3-nitropyrrole

<400> 11
ccaaaaanaa aaagg 15

<210> 12
<211> 12
<212> DNA
<213> Artificial Sequence

<220>
<223> Exemplary nucleotide hybridization sequence used in sequence assembly process

<400> 12
aaaaaatttt tt 12

<210> 13
<211> 12
<212> DNA
<213> Artificial Sequence

<220>
<223> Exemplary nucleotide hybridization sequence used in sequence assembly process

<400> 13
aaaaattttt ta 12

<210> 14
<211> 11
<212> DNA
<213> Artificial Sequence

<220>
<223> Exemplary nucleotide hybridization sequence used in sequence assembly process

a' cont

<400> 14
aaaaattttt t 11

<210> 15
<211> 12
<212> DNA
<213> Artificial Sequence

<220>
<223> Exemplary nucleotide hybridization sequence used in sequence assembly process

<400> 15

aaaaattttt tc 12

<210> 16
<211> 12
<212> DNA
<213> Artificial Sequence

<220>
<223> Exemplary nucleotide hybridization sequence used in sequence assembly process

<400> 16
aaaaattttt tg 12

<210> 17
<211> 12
<212> DNA
<213> Artificial Sequence

<220>
<223> Exemplary nucleotide hybridization sequence used in sequence assembly process

<400> 17
taaaaatttt tt 12

<210> 18
<211> 12
<212> DNA
<213> Artificial Sequence

<220>
<223> Exemplary nucleotide hybridization sequence used in sequence assembly process

<400> 18
caaaaatttt tt 12

<210> 19
<211> 12
<212> DNA
<213> Artificial Sequence

<220>
<223> Exemplary nucleotide hybridization sequence used in sequence assembly process

<400> 19
gaaaaatttt tt 12

<210> 20
<211> 11
<212> DNA
<213> Artificial Sequence

a1 cont

<220>
<223> Exemplary nucleotide hybridization sequence used in sequence assembly process

<400> 20
aaaaaatttt t 11